

## SEQUENCE LISTING

&lt;110&gt; Lukyanov, Sergey

<120> FLUORESCENT PROTEINS FROM COPEPODA SPECIES AND METHODS FOR USING; SAME  
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&lt;160&gt; 30

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1.

&lt;211&gt; 1010

&lt;212&gt; DNA

&lt;213&gt; Pontellina plumata

&lt;400&gt; 1

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&lt;210&gt; 2

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Pontellina plumata

&lt;400&gt; 2

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Ser Gly Thr Leu Asn Gly

1 5 10

15

Val Val Phe Glu Leu Val Gly Gly Glu Gly Ile Pro Glu Gln Gly

20

25

30

Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser  
           35                        40                        45  
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly  
       50                        55                        60  
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ala Asn Asn  
       65                        70                        75                        80  
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val  
       85                        90                        95  
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly  
       100                       105                       110  
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe  
       115                       120                       125  
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro  
       130                       135                       140  
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu  
       145                       150                       155                       160  
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe  
       165                       170                       175  
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Ser Met Phe  
       180                       185                       190  
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile  
       195                       200                       205  
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala  
       210                       215                       220

&lt;210&gt; 3

&lt;211&gt; 1010

&lt;212&gt; DNA

<213> *Pontellina plumata*

&lt;400&gt; 3

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ccccctacct	tctctctcat	gtcatggat	acgggrrcta	ccacttttgtt	acctatccca	240
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gcagggtgt	tggggatttc	aagggtgtcg	ggacaggatt	ccctgaggac	atgtgtatct	420
tcaccgacaa	gatcatccgg	tccaatgcta	ccgtggagca	cttgcacccca	atgggagaca	480
acgttttgtt	gggttcttc	gctgagaacct	ttttccctgag	ggatggaggc	tactactcat	540
ttgtgttgta	cagccacatg	gtgcatcca	cccatccatc	ctccagaacg		600

ggggggcccat gtttgccttc aggagagttg aggaacttca ctccaacact gaacttggca	660
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<210> 4

<211> 222

<212> PRT

<213> Pontellina plumata

<400> 4

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20	25	30	
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser			
35	40	45	
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly			
50	55	60	
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn			
65	70	75	80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val			
85	90	95	
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly			
100	105	110	
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe			
115	120	125	
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro			
130	135	140	
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu			
145	150	155	160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe			
165	170	175	
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe			
180	185	190	
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile			
195	200	205	

Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala  
210 215 220

<210> 5  
<211> 814  
<212> DNA  
<213> *Labidocera aestiva*  
<400> 5

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gatggaaaaca ctgatgaagg acgtatgacc aacaagatga agtccaccaa aggaccttc 180  
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gagggaaaaca aggttatcgg agacttcaag gttgttgat caggattccc agctaacagt 420  
gttatcttca ctgacaagat catcaagtcc aacccaaacct gtgagcacat ctaccccaag 480  
ggagataata ttcttgtaa tgcctacact cgaacttggc tgctgagaga tggtgtgatac ::40  
tactctgcac aggtcaacaa tcatctccac ttcaagactg ccatgcatcc caccatgctc 600  
cagaacggag gatccatgtt tacctacagg aaggttgagg agctccacag ccagtcagat 660  
gttggatattg tagaataacca acatgtcttc aagaccccaa ctgcttttgc ctaagcttgg 720  
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ctcttttaat gaataaaattt ctgtatctac tact 814

<210> 6  
<211> 222  
<212> PRT  
<213> *Labidocera aestiva*  
<400> 6

Gly Gly Tyr Thr Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile  
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 Ile Ser Val Asn Phe Thr Tyr Arg Tyr Glu Gly Asn Lys Val Ile Gly  
                   100                     105                 110  
 Asp Phe Lys Val Val Gly Ser Gly Phe Pro Ala Asn Ser Val Ile Phe  
                   115                     120                 125  
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro  
                   130                     135                 140  
 Lys Gly Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu  
                   145                     150                 155                 160  
 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Leu His Phe  
                   165                     170                 175  
 Lys Thr Ala Met His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe  
                   180                     185                 190  
 Thr Tyr Arg Lys Val Glu Glu Leu His Ser Gln Ser Asp Val Gly Ile  
                   195                     200                 205  
 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala  
                   210                     215                 220

<210> 7  
 <211> 753  
 <212> DNA  
 <213> cf. Pontella meadi Wheeler  
 <400> 7

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 atacagatga gggacgcatg accaacaeee tgaagtccat caaaggacct atctccctct 180  
 ctccctaccc cctctcccac attcttggct acggatatta ccactttgca accttccctg 240  
 ctggatataa aaatatctac cttcatgcca tgaagaatgg aggttactcc aatgtcagaa 300  
 ctgagaggtt tgaggatgga ggcatcattt ctataaccctt caactacaga tatgaaggga 360  
 acaagatcat tggagacttc aaggttggcg gaacaggatt ccctaccaac agtcttatct 420  
 tcactgacaa gatcataaaa tccaaacctt cctgtgagaa catgtcccc aaggctgaca 480  
 atactcttgt gaatgcctac accagaacat atttgcctaa agatggtgga tactactctg 540  
 cccaggtaa caaccatatg cacttcaaga gtgccatcca taccaccatg ctccagaatg 600  
 gcgatccat gttcacctac agagttgttag aggagacaca cactcagaac gaagttgtca 660  
 ttgttagagta ccaaaaatgtc tccaaaactc caactgcgtt tgcttgaaat acttgtata 720  
 aaactgcaaa gaaataaact aaattgtaca atc 753

<210> 8  
 <211> 222

&lt;212&gt; PRT

&lt;213&gt; cf. Pontella meadi Wheeler

&lt;400&gt; 8

Met	Pro	Asp	Met	Lys	Leu	Glu	Cys	His	Ile	Ser	Gly	Thr	Met	Asn	Gly
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Glu	Glu	Phe	Glu	Leu	Ile	Gly	Ala	Gly	Asp	Gly	Asn	Thr	Asp	Glu	Gly
					20				25						30
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Ile	Lys	Gly	Pro	Ile	Ser	Phe	Ser
									35						45
Pro	Tyr	Leu	Leu	Ser	His	Ile	Leu	Gly	Tyr	Gly	Tyr	Tyr	His	Phe	Ala
					50			55							60
Thr	Phe	Pro	Ala	Gly	Tyr	Glu	Asn	Ile	Tyr	Leu	His	Ala	Met	Lys	Asn
					65			70			75				80
Gly	Gly	Tyr	Ser	Asn	Val	Arg	Thr	Glu	Arg	Tyr	Glu	Asp	Gly	Gly	Ile
						85			90						95
Ile	Ser	Ile	Thr	Phe	Asn	Tyr	Arg	Tyr	Glu	Gly	Asn	Lys	Ile	Ile	Gly
					100			105							110
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Thr	Asn	Ser	Leu	Ile	Phe
					115			120							125
Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Thr	Cys	Glu	Asn	Met	Phe	Pro
					130			135							140
Lys	Ala	Asp	Asn	Thr	Leu	Val	Asn	Ala	Tyr	Thr	Arg	Thr	Tyr	Leu	Leu
					145			150			155				160
Lys	Asp	Gly	Gly	Tyr	Tyr	Ser	Ala	Gln	Val	Asn	Asn	His	Met	Phe	
						165			170						175
Lys	Ser	Ala	Ile	His	Thr	Thr	Met	Leu	Gln	Asn	Gly	Ser	Met	Phe	
						180			185						190
Thr	Tyr	Arg	Val	Val	Glu	Glu	Thr	His	Thr	Gln	Asn	Glu	Val	Ala	Ile
					195			200							205
Val	Glu	Tyr	Gln	Asn	Val	Phe	Lys	Thr	Pro	Thr	Ala	Phe	Ala		
					210			215			220				

&lt;210&gt; 9

&lt;211&gt; 880

&lt;212&gt; DNA

&lt;213&gt; cf. Pontella meadi Wheeler

&lt;400&gt; 9

tcctgtgtcc cagtcatcac cggggccctgt gaggaggaag agcacacaga caggagagta	60
taaaatcaga gcggaagcac ggtgatcatc agttccctcag taaacgagta gagacacaca	120

tcaaaaatgcc	tgacatgaag	cttgagtgcc	acatctccgg	aaccatgaat	ggagaggagt	180
ttgaacctat	tggttctgga	gtggaaata	ctgatcaggg	acgcatgaca	aacaatatga	240
agtccatcaa	aggacacctc	tccttctctc	cctacact	ctccccacatt	cttggctatg	300
gatattacca	ctttgcaacc	ttccctgctg	gatatgaaaa	tatcracctt	catgccatga	360
agaatggagg	ttactcaaat	gtcaggactg	agaggtatga	ggatggaggc	atcatttcta	420
taaccccaa	ctacagataat	gaaggcagca	agatcatgg	agacttcaaa	gttatggaa	480
caggatcccc	taccgacag	cttacccatca	ctgacaagat	cataaaatcc	saccctacct	540
gcgagaacat	gttcccccaag	gctgacaaca	ttcttgtgaa	tgccctacacc	agaacctatt	600
tgcttaaaga	tggtgtgatac	tactctgccc	agguttaacaa	ccatatgcac	ttcaagagtg	660
ccatccatcc	tacaatgctc	cagaatggtg	gatccatgtt	cactcacaga	gtagtagagg	720
agaaccacac	taagaccaac	gttgcatacg	tagagtacca	aaatgtcttc	aaaactccca	780
ctgcatttgc	ttaaaaatact	tgttaacaaaa	ctgcaaagaa	ataaacctata	ttgtacaata	840
gcattttat	aatgcataga	aaaataaaatg	tatattttat			880

<210> 10  
<211> 222  
<212> PRT  
<213> cf. *Pontella meadi* Wheeler  
<400> 10

Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe  
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 Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe  
                  180                     185                     190  
 Thr His Arg Val Val Glu Glu Asn His Thr Lys Thr Asn Val Ala Ile  
                  195                     200                     205  
 Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala  
                  210                     215                     220

&lt;210&gt; 11

&lt;211&gt; 847

&lt;212&gt; DNA

&lt;213&gt; Pontella mediterranea

&lt;400&gt; 11

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 tttgaaccttgc ttgggtgtgg agaaggaaac actgtatgagg gacgcattgac caacaagatg     180  
 aagtccacca agggacccctt ttcctttctt ccttatttgc tctccccacgt tcttggttat     240  
 ggatactacc actatgttac ctccctgtct ggatatgaaa atgttacccctt ccattgcattg     300  
 aagaatggag gtttactccaa cacaagaact gagaggtatg aggatggagg tatcatttctt     360  
 gtttacccca actacagata tgaagggaga cagatttcatg gagacttcaa gtttggtagga     420  
 acgggattcc ctggccgacag catcatcttcc actgacaaga tcaatcaagtc caacccttacc     480  
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 gagttccaca cacaaactga agtcggattt gtttgaatacc agcatgtttt caagaggccaa     720  
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 aaaaaaaaaaaaaaaa     847

&lt;210&gt; 12

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Pontella mediterranea

&lt;400&gt; 12

Met Pro Asn Met Lys Leu Glu Cys Arg Ile Ser Gly Thr Met Asn Gly  
     1                 5                     10                     15  
 Glu Glu Phe Glu Glu Val Gly Ala Gly Glu Gly Asn Thr Asp Glu Gly  
     20                 25                     30

Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser  
 35 40 45  
 Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala  
 50 55 60  
 Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn  
 65 70 75 80  
 Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile  
 85 90 95  
 Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly  
 100 105 110  
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe  
 115 120 125  
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro  
 130 135 140  
 Lys Ala Asn Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu  
 145 150 155 160  
 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Leu  
 165 170 175  
 Gln Ser Ala Ile His Pro Thr Met Leu Lys Asn Gly Gly Ser Met Phe  
 180 185 190  
 Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala  
 210 215 220

<210> 13  
 <211> 850  
 <212> DNA  
 <213> Pontella mediterranea  
 <400> 13

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tttgaacttg	ttggtgctgg	agatggaaac	actgatgagg	gacgcattgac	caaccagatg	180
aagtccacaa	agggacctct	ctccttctct	ccctacttgc	tctcccacgt	tcttggctat	240
ggataactacc	actatgttac	cttccctgct	ggatatgaaa	atgtcttccct	ccatgccatg	300
aagaatggag	gttactccaa	cacaagaact	gagaggatg	acgatggagg	tatcatttct	360
gctaccccca	actacagata	tgaagggaga	cagattcatg	gagacttcaa	ggttgttggaa	420
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tgtgagcaca	tctaccccaa	ggctgacaat	attcttgtga	atgcctacac	cagaacctgg	510
atgccttagag	atggtggtata	ctactctgtt	caggtcaaca	accacatgca	ctttaagagt	600

gccatccatc ccaccatgtt ccagaatgggt ggatctatgt tcacctacag aaaggtttag	660
gagctccaca cacaaactga agttggattt gttgagtacc agcatgtttt caagaggccc	720
acagcttttg cttaattttg taaataaaga aagaatttat aatacaatag tgctttatg	780
tttctaaaac aatgaatgtt taaataaaatc tcaaaaatatt caaaaaaaaaaaaaaaa	840
aaaaaaaaaaa	850

<210> 14  
 <211> 222  
 <212> PRT  
 <213> Pontella mediterranea  
 <400> 14

Met Pro His Met Lys Leu Glu Cys Arg Ile Ser Gly Thr Met Asn Gly			
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Glu Glu Phe Glu Leu Val Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly			
20	25	30	
Arg Met Thr Asn Gln Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser			
35	40	45	
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala			
50	55	60	
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn			
65	70	75	80
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Asp Asp Gly Gly Ile			
85	90	95	
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly			
100	105	110	
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe			
115	120	125	
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro			
130	135	140	
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu			
145	150	155	160
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe			
165	170	175	
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe			
180	185	190	
Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile			
195	200	205	
Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala			
210	215	220	

&lt;210&gt; 15

&lt;211&gt; 821

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

<223> nucleic acid sequence for pdaelGFP from an unidentified  
Pontellidae species, complete cds

&lt;400&gt; 15

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ggaaatactg	atcagggACG	tatgaccaac	aagatgaaAT	ctaccaAGGG	tccactCTCC	180
tTCTCTCCCT	ATCTTCTCTC	TCAATGTATG	GGATATGGAT	TCTATCATTT	TGGAACATTT	240
CCCAGTGGTT	ATGAGAAATCC	CTATGTCAC	GCCATGACGA	ACGGTGGATA	TACCAACACC	300
aggattgaaa	GTATGAAGA	TGGAGGTGTT	CTTACCTTA	CCTTCAACTA	CAGATTGGAT	360
ggaaacaaga	TTATCGGGGA	CTTCAAGTGT	GTCGGAACTG	GATTCCCTGA	GGACAGCGTT	420
ATCTTCACtg	AACAAGATCAT	CAAGTCCAAC	CCCAATTGtg	AACATTCTTA	TCCAATGGCT	480
gaaaacatca	TGAAAAATGC	CTACATGAGA	ACTCTCTCCC	TCAAGAGATGG	TGGCTACTAC	540
TCTGGCCAGG	TTACCAAGCCA	CATCCACTTC	AAGAAATGCGA	TCCACCCATC	CATCCTTCAT	600
AACGGCGGAT	CCATGTCAC	CTACAGAAAGA	GTTGAGGAGC	TCCACACTCA	AACTGATCTT	660
GGAAATGTTG	AGTACCAAGCA	TGTATTCAAG	ACTCCCACtg	CTTTGCTTG	AATGCCATGA	720
AGATGAAACC	TGAACAAAGAT	CAATCTTAT	TTACCAACAAT	ATGAAATGTA	TTAATTGTA	780
TAATTCTCGA	GAATTCAAT	AATACATAGA	ATTATCTTA	C		821

&lt;210&gt; 16

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

<223> amino acid sequence for pdaelGFP from an unidentified Pontellidae  
species

&lt;400&gt; 16

Met	Ala	Ala	Met	Lys	Ile	Glu	Cys	Arg	Ile	Thr	Gly	Thr	Met	Asn	Gly
1				5					10				15		
Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly	Glu	Gly	Asn	Thr	Asp	Gln	Gly
					20				25				30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Pro	Leu	Ser	Phe	Ser
					35				40			45			
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly
					50			55			60				

Thr	Phe	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Tyr	Val	His	Ala	Met	Thr	Asn
65				70				75				80			
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Ser	Tyr	Glu	Asp	Gly	Gly	Val
				85				90				95			
Leu	Tyr	Leu	Thr	Phe	Asn	Tyr	Arg	Leu	Asp	Gly	Asn	Lys	Ile	Ile	Gly
				100				105				110			
Asp	Phe	Lys	Cys	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile	Phe
				115				120				125			
Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Asn	Cys	Glu	His	Phe	Tyr	Pro
				130				135				140			
Met	Ala	Glu	Asn	Ile	Met	Lys	Asn	Ala	Tyr	Met	Arg	Thr	Leu	Ser	Leu
				145				150				155			160
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Gly	Gln	Val	Thr	Ser	His	Ile	His	Phe
				165				170				175			
Lys	Asn	Ala	Ile	His	Pro	Ser	Ile	Leu	His	Asn	Gly	Gly	Ser	Met	Phe
				180				185				190			
Thr	Tyr	Arg	Arg	Val	Glu	Glu	Leu	His	Thr	Gln	Thr	Asp	Leu	Gly	Ile
				195				200				205			
Val	Glu	Tyr	Gln	His	Val	Phe	Lys	Thr	Pro	Thr	Ala	Phe	Ale		
				210				215				220			

&lt;210&gt; 17

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for the humanized version of the pplugFPR

&lt;400&gt; 17

atgccccgcca	tgaagatcga	gtgccgcatac	accggcacccc	tgaacggcggt	ggaggttcgag	60
ctgggtggcg	gcggagaggg	caccccccgg	caggggccgca	tgaccaaaca	aatgaagagc	120
accaagggcg	ccctgaccc	cagccccctac	ctgtgtgagcc	acgtgtatggg	ctacggcttc	180
taccacttgc	gcacacctacc	cagcggtctac	gagaacccct	tcctgcacgc	catcaacaac	240
ggcggctaca	ccaacacccg	catcgagaag	tacgaggacg	gcggcggtgt	gcacgtgagc	300
ttcagctacc	gctacgaggc	cggccgcgtg	atcggcgact	tcaagggtgggt	gggcacccggc	360
ttccccggagg	acagcgtgtat	tttcacccgac	aagatcatcc	gcagcaacgc	caccgtggag	420
cacctgcacc	ccatgggcga	taacgtgttg	gtgggcagct	tcccccgcac	tttcagcctg	480
cgcgacggcg	gtctactacag	tttcgtgggt	gacagccaca	tgcacttcaa	gagcgcacatc	540
caccccaagca	ttctgcagaa	cggggggcccc	atgttcgcct	tccgcccgcgt	ggaggagctg	600
cacagcaaca	ccgagctgggg	catcggtggag	taccagcaccg	ccttcagagac	cccgcacgc	660
ttcgccctga						669

<210> 18  
 <211> 222  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> amino acid sequence for the humanized version of the ppiuGFP2  
 <400> 18

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly  
 1 5 10 15  
 Val Glu Phe Glu Leu Val Gly Gly Glu Gly Thr Pro Glu Gln Gly  
 . 20 25 30  
 Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser  
 35 40 45  
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly  
 50 55 60  
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn  
 65 70 75 80  
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val  
 85 90 95  
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly  
 100 105 110  
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe  
 115 120 125  
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro  
 130 135 140  
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu  
 145 150 155 160  
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe  
 165 170 175  
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe  
 180 185 190  
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala  
 210 215 220

<210> 19  
 <211> 589  
 <212> DNA  
 <213> Artificial sequence

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for the ppluGFP2 with yeast-optimized codon usage

&lt;400&gt; 19

tactccagaa	caaggtagaa	tgactaataa	aatgaaaatct	actaaaggcg	ctttgcactt	60
ttctccatat	ttgttgtctc	atgttatggg	ttatggttt	tatcattttg	gtacttaccc	120
atctggttat	aaaaatccat	ttttgcatgc	tattaataat	ggtgggtata	ctaatactag	180
aattgaaaaa	catgaagatg	gtgggtttt	gcatgtttct	ttttttata	gatatgaagc	240
tggtagagtt	attggcgatt	ttaaagtgt	tggtaactgg	tttccagaag	attctgttat	300
ttttactgat	aaaattatta	gatctaattgc	tactgttcaa	catttgcattc	caatgggtga	360
taatgtttt	gttggtttt	ttgttagaac	tttttttttgc	agagatgg	gttattatcc	420
ttttgttgtt	gattctcata	tgcattttaa	atctgctatt	cattccatcta	ttttgcacaaa	480
tggtaggtcca	atgtttgcctt	ttagaagatg	tgaagaattg	cattctaaata	ctgaattggg	540
tattgttcaa	catcaacatg	ctttttaaaac	tccaaattgt	tttgcttaa		589

&lt;210&gt; 20

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; amino acid sequence for the ppluGFP2 with yeast-optimized codon usage

&lt;400&gt; 20

Met	Pro	Ala	Met	Lys	Ile	Glu	Cys	Arg	Ile	Thr	Gly	Thr	Leu	Asn	Gly		
1				5										10		15	
Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Glu	Gly	Thr	Pro	Glu	Gln	Gly			
					20					25				30			
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe	Ser		
					35				40				45				
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly		
					50			55			60						
Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Phe	Leu	His	Ala	Ile	Asn	Asn		
					65				70		75			80			
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Lys	Tyr	Glu	Asp	Gly	Gly	Val		
						85			90				95				
Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	Glu	Ala	Gly	Arg	Val	Ile	Gly		
						100			105			110					
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile	Phe		
					115				120			125					

Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro  
 130 135 140  
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu  
 145 150 155 160  
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe  
 165 170 175  
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe  
 180 185 190  
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala  
 210 215 220

&lt;210&gt; 21

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for the CopCFP mutant

&lt;400&gt; 21

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atgcccgcga tgaagatcga gtgccgcata accggcaccc tgaacggcggt ggaggttcgag 60
ctgggtggcg gcgaggagggg caccccccgag cagggccgcga tgaccaacaa gatgaagagc 120
accaaaggcg ccctgacctt cagccccatc ctgttgagcc acgtgtatggg ctggggcttt 180
taccacttcg gcacctatccc cagcggtatc gagaacccct tcctgcacgc catcaacaac 240
ggcggttaca ccaacacccg catcgagaag tacgaggacg goggcggtgc gcacgtgagc 300
ttcagctacc gctacgagggc cggccgcgtg atcggcgact tcaagggtggt gggcaccggc 360
ttccccgagg acagcggtat cttcaccgcac aagatcatcc gcagcaacgc caccgtggag 420
cacctgcgcc ccatgggcga taacgtgtcg gtggggcagct tcggccgcac cttcagcctg 480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc 540
cacccccagca tcctgcagaa cggggggcccc atgttgcct tccggccgcgt ggaggagctg 600
cacagcaaca ccgagctggg catcggtggag taccagcacg ctttcaagac cccgaccgc 660
ttcgccctaa 669
  
```

&lt;210&gt; 22

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; amino acid sequence for the CopCFP mutant

&lt;400&gt; 22

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly  
 1 5 10 15  
 Val Glu Phe Glu Leu Val Gly Gly Glu Gly Thr Pro Glu Gln Gly  
 20 25 30  
 Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser  
 35 40 45  
 Pro Tyr Leu Leu Ser His Val Met Gly Trp Gly Phe Tyr His Phe Gly  
 50 55 60  
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn  
 65 70 75 80  
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val  
 85 90 95  
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly  
 100 105 110  
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe  
 115 120 125  
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu Arg Pro  
 130 135 140  
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu  
 145 150 155 160  
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe  
 165 170 175  
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe  
 180 185 190  
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala  
 210 215 220

&lt;210&gt; 23

&lt;211&gt; 690

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for the CopGFP-NAL variant

&lt;400&gt; 23

atggagagcg acgagagccg cctgcggcc	atggagatcg agtgccgcat caccggcacc	60
ctgaacggcg tggagttcga gctgggtggc ggccggagagg gcaccccccga	gcagggccgc	120
atgaccaaca agatgaagag caccaagggc gccccgacct tcagcccccta	cctgcgtgagc	180
cacgtgtatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta	cgagaacccc	240

tccctgcacg	ccatcaacaa	cggcggctac	accaacaccc	gcatcgagaa	gtacgaggac	300
ggcggcgtgc	tgcacgtgag	cttcagctac	cgctacgagg	cggccgcgt	gatcgccgac	360
ttcaagggtgg	tgggcacccgg	cttccccgag	gacagcgtga	tcttaccga	caagatcatc	420
cgcagcaacg	ccaccgtgga	gcacccgtcac	cccattggcg	ataacgtgt	ggtgggcagc	480
tccgccccca	ccttcagcct	gcgcgacggc	ggctactaca	gcrrcggt	ggacagccac	540
atgcacttca	agagcgccat	ccacccca	atccgcaga	acgggggccc	catgttcgcc	600
tcccgccgcg	tggaggagct	gcacageaac	accgagctgg	gcattcgta	gtaccagcac	660
gccttcaaga	ccccgatcgc	attcgccctga				690

&lt;210&gt; 24

&lt;211&gt; 229

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; amino acid sequence for the CopGFP-NAL variant

&lt;400&gt; 24

Met	Glu	Ser	Asp	Glu	Ser	Gly	Leu	Pro	Ala	Met	Glu	Ile	Glu	Cys	Arg		
1										5				10		15	
Ile	Thr	Gly	Thr	Leu	Asn	Gly	Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly		
														20	25	30	
Glu	Gly	Thr	Pro	Glu	Gln	Gly	Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr		
														35	40	45	
Lys	Gly	Ala	Leu	Thr	Phe	Ser	Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly		
														50	55	60	
Tyr	Gly	Phe	Tyr	His	Phe	Gly	Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro		
														65	70	75	80
Phe	Leu	His	Ala	Ile	Asn	Asn	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu			
														85	90	95	
Lys	Tyr	Glu	Asp	Gly	Gly	Val	Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr		
														100	105	110	
Glu	Ala	Gly	Arg	Val	Ile	Gly	Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe		
														115	120	125	
Pro	Glu	Asp	Ser	Val	Ile	Phe	Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala		
														130	135	140	
Thr	Val	Glu	His	Leu	His	Pro	Met	Gly	Asp	Asn	Val	Leu	Val	Gly	Ser		
														145	150	155	160
Phe	Ala	Arg	Thr	Phe	Ser	Leu	Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Phe	Val		
														165	170	175	
Val	Asp	Ser	His	Met	His	Phe	Lys	Ser	Ala	Ile	His	Pro	Ser	Ile	Leu		
														180	185	190	

Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His		
195	200	205
Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr		
210	215	220

Pro Ile Ala Phe Ala

225

<210> 25

<211> 819

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA2 variant

<400> 25

atgcccccca tgaagatcga gtgccgcatac accggcaccc tgaacggcggt ggaggttcgag	60
ctggcgggcg gcggagaggg caccccccag cagggccgca tgaccaaaca gatgaagagc	120
accaaggggcg ccctgaccctt cagcccc tac ctgctgagcc acgtgtatggg ctacggcttc	180
taccacttcg gcacctaacc cagcggtac gagaacccct tcctgcacgc catcaacaac	240
ggcggtacca ccaacaccccg catcgagaag tacgaggacg gcggcgtgt gcacgtgagc	300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaagggttgt gggcacccggc	360
ttcccccaggc acagcggtat ctccaccgac aagatcatcc gcagcaacgc caccgtggag	420
caccgtgcacc ccatgggcga taacgtgttg gtgggcagct tcgccccgac cttagccctg	480
cgcgacggcg gtcactacag ctctcggttg gacagccaca tgcacttcaa gagcgccatc	540
caccccccaga tccctgcagaa cgggggcccc atgttcgcct tccgcgcgtt ggaggagctg	600
cacagcaaca ccgagctggg catcggtggag taccagcact cttcaagac cccgatcgca	660
ttcgccagat ccagagccca ggcgcagcaac tccgcgtgg atggcacagc cggaccggga	720
tcggccgcga ctctagatca taatcagcca taccacattt ttagaggtt tacttgcctt	780
aaaaaacctc ccacacccccc ccctgaacct gaaacataaa	819

<210> 26

<211> 272

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA2 variant

<400> 26

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly

1

5

10

15

Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly  
           20                       25                       30  
 Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser  
           35                       40                       45  
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly  
           50                       55                       60  
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn  
   65                       70                       75                       80  
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val  
           85                       90                       95  
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly  
           100                       105                       110  
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe  
           115                       120                       125  
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro  
           130                       135                       140  
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu  
   145                       150                       155                       160  
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe  
           165                       170                       175  
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe  
           180                       185                       190  
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile  
           195                       200                       205  
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala Arg Ser  
           210                       215                       220  
 Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly Pro Gly  
   225                       230                       235                       240  
 Ser Ala Ala Thr Leu Asp His Asn Gln Pro Tyr His Ile Cys Arg Gly  
           245                       250                       255  
 Phe Thr Cys Phe Lys Lys Pro Pro Thr Pro Pro Pro Glu Pro Glu Thr  
           260                       265                       270

&lt;210&gt; 27

&lt;211&gt; 840

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for the CopGFP-NA3 variant

&lt;400&gt; 27

atggagagcg acgagagccg cctgaccgcgc atggagatcg agtgccgcat caccggcacc

60

ctgaaacggcg	tggagttcga	gtgggtggc	ggcggagagg	gcaccccccga	gcagggccgc	120
atgaccaaca	agatgaagag	caccaaggc	gccctgacct	ttagccccct	cctgctgagc	180
cacgtgatgg	gtcacggctt	ctaccacttc	ggcacccacc	ccagcggcta	cgagaacccc	240
ttcctgcacg	ccatcaacaa	cggcggctac	accaacaccc	gcatcgagaa	gtacgaggac	300
ggcggcggtgc	tgcacgtgag	cttcagctac	cgctacgagg	ccggccgcgt	gatccggcgcac	360
ttcaagggtgg	tgggcacccgg	cttccccgag	gacagcgtga	tcttcaccga	caagatccatc	420
cgcagcaacg	ccaccgttgg	gcacctgcac	cccatggggcg	ataacgtgt	ggtgggcagc	480
ttcggcccgca	ccttcagctt	gogcgacggc	ggctactaca	gcttcgtggc	ggacagccac	540
atgcacttca	agagcgccat	ccacccccc	atccctgcaga	acggggggccc	catgttcgccc	600
ttccggcccg	tggaggagct	gcacagcaac	accgagctgg	gcategtgg	gtaccagcac	660
gccttcaaga	ccccgatcgc	atccggcaga	tccagagccc	aggccagcaa	ctccggccgtg	720
gatggcacag	ccggaccggg	atccggcccg	actctagatc	ataatcagcc	ataccacatt	780
tgttagaggtt	ttacttgott	taaaaaacct	cccacaccc	cccttgaacc	tgeaacataa	840

&lt;210&gt; 28

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; amino acid sequence for the CopGFP-NA3 variant

&lt;400&gt; 28

Met	Glu	Ser	Asp	Glu	Ser	Gly	Ile	Leu	Pro	Ala	Met	Glu	Ile	Glu	Cys	Arg
1				5							10				15	
Ile	Thr	Gly	Thr	Leu	Asn	Gly	Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly	
				20				25				30				
Glu	Gly	Thr	Pro	Glu	Gln	Gly	Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	
				35			40				45					
Lys	Gly	Ala	Leu	Thr	Phe	Ser	Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	
				50			55				60					
Tyr	Gly	Phe	Tyr	His	Phe	Gly	Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	
				65			70			75			80			
Phe	Leu	His	Ala	Ile	Asn	Asn	Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	
				85			90				95					
Lys	Tyr	Glu	Asp	Gly	Gly	Val	Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	
				100			105				110					
Glu	Ala	Gly	Arg	Val	Ile	Gly	Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	
				115			120				125					
Pro	Glu	Asp	Ser	Val	Ile	Phe	Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala	
				130			135			140						

Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser  
 145 150 155 160  
 Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val  
 165 170 175  
 Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu  
 180 185 190  
 Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His  
 195 200 205  
 Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr  
 210 215 220  
 Pro Ile Ala Phe Ala Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val  
 225 230 235 240  
 Asp Gly Thr Ala Gly Pro Gly Ser Ala Ala Thr Leu Asp His Asn Gln  
 245 250 255  
 Pro Tyr His Ile Cys Arg Gly Phe Thr Cys Phe Lys Lys Pro Pro Thr  
 260 265 270  
 Pro Pro Pro Glu Pro Glu Thr  
 275

<210> 29  
 <211> 238  
 <212> PRT  
 <213> Aequorea victoria

<400> 29

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
 65 70 75 80  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

115	120	125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130	135	140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
145	150	155
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		
165	170	175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
180	185	190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
195	200	205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		
210	215	220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys		
225	230	235

<210> 30  
<211> 225  
<212> PRT  
<213> Discosoma sp.

<400> 30

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val		
1	5	10
Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu		
20	25	30
Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val		
35	40	45
Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln		
50	55	60
Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro		
65	70	75
Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val		
85	90	95
Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser		
100	105	110
Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn		
115	120	125
Phe Pro Ser Asp Gly Pro Val-Met Gln Lys Lys Thr Met Gly Trp Glu		
130	135	140

Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu  
145 150 155 160  
Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu  
165 170 175  
Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr  
180 185 190  
Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr  
195 200 205  
Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe  
210 215 220  
Leu  
225